

WEST Search History

Hide Items

Restore

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DATE: Tuesday, September 26, 2006

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L5	tanaguchi-na\$.in.	1
<input type="checkbox"/>	L4	l1 and L3	3
<input type="checkbox"/>	L3	800/8,9,13,18.ccls.	2495
<input type="checkbox"/>	L2	L1 and (knockout or recombination or transgenic)	69
<input type="checkbox"/>	L1	FUT8 or (1,6 fucosyltransferase)	91

END OF SEARCH HISTORY

(FILE 'HOME' ENTERED AT 15:29:51 ON 26 SEP 2006)

FILE 'CAPLUS, MEDLINE, EMBASE, BIOSIS, LIFESCI' ENTERED AT 15:30:08 ON 26 SEP 2006

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L1      346 S 1,6FUCOSYLTRANSFERASE OR (1,6 FUCOSYLTRANSFERASE) OR (FUT8)
L2      75 S 1L AND (KNOCKOUT OR TRANSGEN?)
L3      57 S L2 AND (MOUSE OR MURINE)
L4      36 S L3 AND PY<=2002
L5      21 DUP REM L4 (15 DUPLICATES REMOVED)
L6      2 S TANAGUCHI N?/AU
L7      2 DUP REM L6 (0 DUPLICATES REMOVED)
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GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2006, 05:02:29 ; Search time 1116 Seconds
(without alignments)
10795.740 Million cell updates/sec

Title: US-10-803-100-2
Perfect score: 1728
Sequence: 1 atgcgggcatggactgggttc.....atcctgaagctgaaaaatag 1728

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1728	100.0	1728	6	ABK70032	Abk70032 Antibody
2	1728	100.0	1728	10	ADC66321	Adc66321 Mouse gen
3	1728	100.0	1728	10	ADE73053	Ade73053 Murine FU
4	1728	100.0	1728	10	ADL18089	Adl18089 Anti-lect
5	1728	100.0	1728	11	ADL35245	Adl35245 Murine an
6	1728	100.0	1728	13	ADT88117	Adt88117 Mouse (al
7	1728	100.0	1728	14	ADZ59300	Adz59300 Mouse alp
8	1728	100.0	1728	14	ADZ58511	Adz58511 VEGF rece
9	1728	100.0	1728	14	ADZ57766	Adz57766 Mouse alp
10	1728	100.0	1728	14	ADZ69205	Adz69205 IL-5R alp
11	1728	100.0	1728	14	ADZ52571	Adz52571 Mouse ant

12	1728	100.0	1728	14	ADZ57802	Adz57802	Gangliosi
13	1728	100.0	1728	14	ADZ48261	Adz48261	Pharmaceu
14	1728	100.0	1728	14	ADZ59877	Adz59877	Glycoprot
15	1728	100.0	1728	14	ADZ52525	Adz52525	Mouse CCR
16	1728	100.0	1728	14	AEC08751	Aec08751	Mouse alp
17	1728	100.0	3052	15	AEF70393	Aef70393	Mouse GDP
18	1656	95.8	1728	15	AEF70394	Aef70394	Rat GDP-m
19	1584	91.7	2008	6	ABK70031	Abk70031	Antibody
20	1584	91.7	2008	10	ADC66320	Adc66320	Chinese h
21	1584	91.7	2008	10	ADE73052	Ade73052	Hamster F
22	1584	91.7	2008	10	ADL18088	Adl18088	Anti-lect
23	1584	91.7	2008	11	ADL35244	Adl35244	Chinese h
24	1584	91.7	2008	14	ADZ59299	Adz59299	Chinese h
25	1584	91.7	2008	14	ADZ58510	Adz58510	VEGF rece
26	1584	91.7	2008	14	ADZ57765	Adz57765	Chinese h
27	1584	91.7	2008	14	ADZ69204	Adz69204	IL-5R alp
28	1584	91.7	2008	14	ADZ52570	Adz52570	Chinese h
29	1584	91.7	2008	14	ADZ57801	Adz57801	Gangliosi
30	1584	91.7	2008	14	ADZ48260	Adz48260	Pharmaceu
31	1584	91.7	2008	14	ADZ59876	Adz59876	Glycoprot
32	1584	91.7	2008	14	ADZ52524	Adz52524	Chinese h
33	1584	91.7	2008	15	AEF70392	Aef70392	GDP-manno
34	1578.2	91.3	1728	14	ADY53562	Ady53562	Chinese h
35	1568.6	90.8	1728	10	ADF42498	Adf42498	Chinese h
36	1501.4	86.9	1728	10	ADL18091	Adl18091	Anti-lect
37	1501.4	86.9	1728	14	ADZ59302	Adz59302	Human alp
38	1501.4	86.9	1759	6	ABA98809	Aba98809	Alphal,6-
39	1501.4	86.9	2002	10	ADC64482	Adc64482	Human inh
40	1501.4	86.9	2100	2	AAT76574	Aat76574	Human alp
41	1501.4	86.9	2902	15	AEF70395	Aef70395	Human GDP
42	1501.4	86.9	3280	13	ADR25185	Adr25185	Breast ca
43	1501.4	86.9	3280	14	ADY61814	Ady61814	Human gen
44	1501.4	86.9	3280	15	AEE84862	Aee84862	IMPDH mar
45	1501.4	86.9	3291	5	ABV22468	Abv22468	Human pro

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2006, 05:12:20 ; Search time 7506 Seconds
(without alignments)
12873.515 Million cell updates/sec

Title: US-10-803-100-2
Perfect score: 1728
Sequence: 1 atgcgggcatggactggttc.....atcctgaagctgaaaaatag 1728

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1728	100.0	2766	6	AK051811	AK051811 Mus muscu
2	1728	100.0	3052	6	AK048520	AK048520 Mus muscu
3	1724.8	99.8	3358	6	AK134537	AK134537 Mus muscu
4	1710	99.0	1724	14	AY410162	AY410162 Mus muscu
5	1499.8	86.8	1987	6	CR617923	CR617923 full-leng
6	1497.4	86.7	1728	14	AY410160	AY410160 Homo sapi
7	1476.6	85.5	3036	6	CR926471	CR926471 Pongo pyg
8	1431.6	82.8	1711	14	AY410161	AY410161 Pan trogl
9	913.2	52.8	937	3	BQ892101	BQ892101 AGENCOURT
10	837.4	48.5	2210	6	AK163494	AK163494 Mus muscu
11	801.6	46.4	898	4	CB194828	CB194828 AGENCOURT
12	787.6	45.6	1066	3	BM928521	BM928521 AGENCOURT

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	13	754.6	43.7	802	5	CF749007	CF749007	UI-M-HJ0-
	14	750	43.4	752	5	CD807939	CD807939	UI-M-GW0-
	15	747.2	43.2	940	3	BQ653329	BQ653329	AGENCOURT
	16	746.8	43.2	900	4	BX452321	BX452321	BX452321
	17	735.2	42.5	886	3	BQ423860	BQ423860	AGENCOURT
	18	725	42.0	898	4	BX429921	BX429921	BX429921
	19	720.4	41.7	855	3	BU184296	BU184296	AGENCOURT
	20	704.6	40.8	937	3	BU513162	BU513162	AGENCOURT
	21	696.8	40.3	963	4	BX450010	BX450010	BX450010
	22	693.2	40.1	893	10	DT807919	DT807919	LB0173.CR
	23	687.4	39.8	834	1	AU124128	AU124128	AU124128
	24	665.4	38.5	723	8	CX216966	CX216966	MNS30886
	25	660.2	38.2	702	2	BG973221	BG973221	602842563
	26	656	38.0	656	3	BQ552954	BQ552954	H4019B10-
	27	644.2	37.3	785	8	CO568375	CO568375	AGENCOURT
	28	627.2	36.3	752	3	BQ604588	BQ604588	MI-P-CP1-
C	29	627.2	36.3	754	4	BX414472	BX414472	BX414472
	30	621.8	36.0	647	5	CD772615	CD772615	AGENCOURT
	31	620.2	35.9	965	2	BI546364	BI546364	603188856
	32	618.8	35.8	703	9	CX784163	CX784163	HESC3_30_
	33	615.6	35.6	753	8	CV109889	CV109889	AGENCOURT
	34	615.2	35.6	790	4	CB989769	CB989769	AGENCOURT
	35	613	35.5	613	4	CA539475	CA539475	C0279D08-
	36	610.8	35.3	840	5	CD653052	CD653052	AGENCOURT
	37	608.8	35.2	692	4	CB105611	CB105611	K-EST0130
	38	608.8	35.2	692	4	CB105621	CB105621	K-EST0130
	39	593	34.3	805	4	CA489662	CA489662	AGENCOURT
C	40	592.8	34.3	717	4	CB322023	CB322023	UI-CF-FN0
	41	590.2	34.2	828	5	CJ469991	CJ469991	CJ469991
	42	587.6	34.0	675	4	BX952151	BX952151	DKFZp781H
	43	584.6	33.8	890	9	CX406578	CX406578	JGI_XZT61
	44	576.4	33.4	769	2	BG501191	BG501191	602546241
	45	572.6	33.1	889	4	BX734333	BX734333	BX734333

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2006, 05:04:59 ; Search time 9812 Seconds
(without alignments)
11261.837 Million cell updates/sec

Title: US-10-803-100-2
Perfect score: 1728
Sequence: 1 atgcgggcatggactggttc.....atcctgaagctgaaaaatag 1728

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	1728	100.0	1728	2	BD168517	BD168517 Cells pro
	2	1728	100.0	1728	2	AR721184	AR721184 Sequence
	3	1728	100.0	2976	6	BC010666	BC010666 Mus muscu

4	1723.2	99.7	2176	6	AB025198	AB025198 Mus muscu
5	1656	95.8	1728	6	AJ781406	AJ781406 Rattus no
6	1584	91.7	2008	2	BD168516	BD168516 Cells pro
7	1584	91.7	2008	2	AR721183	AR721183 Sequence
8	1506.2	87.2	1728	14	AJ830717	AJ830717 Canis fam
9	1501.4	86.9	1728	5	AJ781405	AJ781405 Pan trogl
10	1501.4	86.9	1759	2	BD087745	BD087745 Plant cel
11	1501.4	86.9	1759	2	AX662735	AX662735 Sequence
12	1501.4	86.9	2002	2	BD187624	BD187624 Screening
13	1501.4	86.9	2002	5	D89289	D89289 Homo sapien
14	1501.4	86.9	2100	2	E15725	E15725 Human mRNA
15	1501.4	86.9	2787	2	CQ719867	CQ719867 Sequence
16	1501.4	86.9	2796	5	HSA539535	AJ539535 Homo sapi
17	1501.4	86.9	2898	5	HSY17976	Y17976 Homo sapien
18	1501.4	86.9	2902	5	HSA539536	AJ539536 Homo sapi
19	1501.4	86.9	2992	5	HSY17977	Y17977 Homo sapien
20	1501.4	86.9	3186	5	HSY17978	Y17978 Homo sapien
21	1501.4	86.9	3280	5	HSY17979	Y17979 Homo sapien
22	1501.4	86.9	3291	2	CQ490594	CQ490594 Sequence
23	1501.4	86.9	3291	2	CQ496429	CQ496429 Sequence
24	1501.4	86.9	3568	5	HSA536055	AJ536055 Homo sapi
25	1501.4	86.9	3666	5	HSA536053	AJ536053 Homo sapi
26	1501.4	86.9	3772	5	HSA536054	AJ536054 Homo sapi
27	1501.4	86.9	4196	5	HSA536056	AJ536056 Homo sapi
28	1496.6	86.6	2100	2	AR170077	AR170077 Sequence
29	1482.2	85.8	2546	14	BC104555	BC104555 Bos tauru
30	1472.6	85.2	1728	14	AF247186	AF247186 Bos tauru
31	1469.4	85.0	1728	2	AR170074	AR170074 Sequence
32	1469.4	85.0	1728	2	E14720	E14720 Procine mRN
33	1469.4	85.0	1836	14	D86723	D86723 Porcine mRN
34	1320.2	76.4	1695	2	DD183551	DD183551 A crystal
35	1214.4	70.3	1728	11	AJ830718	AJ830718 Gallus ga
36	1208	69.9	2677	5	BC025385	BC025385 Homo sapi
37	1208	69.9	2682	2	CS031521	CS031521 Sequence
38	1208	69.9	2682	2	CS040473	CS040473 Sequence
39	1093	63.3	2785	11	BC067957	BC067957 Xenopus t
40	1091.4	63.2	2208	11	BC079978	BC079978 Xenopus l
41	1088.2	63.0	2129	11	XLA514872	AJ514872 Xenopus l
42	1055	61.1	2556	11	AJ721048	AJ721048 Gallus ga
43	941	54.5	1850	5	AF052088	AF052088 Homo sapi
44	931	53.9	979	2	BD168522	BD168522 Cells pro
45	931	53.9	979	2	AR721189	AR721189 Sequence